

Fig. 1A

SUS1	SEQ ID NO: 42	ENGILRKWISRFDVWPYL	native
SUS2	SEQ ID NO: 3	ENGIVRKWISRFEVWPYL	native
SS2	SEQ ID NO: 10	GIVRKWISRFEVWPYLKK	active
SS11	SEQ ID NO: 11	ILRVPFRTENGIVRKWI(NH2)	inactive
SS12	SEQ ID NO: 12	GIVRKWISRFEVWPYL(NH2)	active
SS15	SEQ ID NO: 13	GIVRKWISRFEVAPYL(NH2)	less active
SS16	SEQ ID NO: 14	SRFEVWPYL(NH2)	less active
SP3	SEQ ID NO: 18	NRRISSVE N NDKK(NH2)	inactive
NR11	SEQ ID NO: 15	GPTLKRFASTAFMNTTSKK	inactive
SP26	SEQ ID NO: 16	GRMRRIATVEMMKK	inactive
SS1	SEQ ID NO: 9	GDRVLSRLHSVRERIGK	inactive
ACTIN	SEQ ID NO: 19	EHGIVTNWDDMEKIWHHTFY	consensus

Double basic cluster: black box; e.g. **KK**

Possible region of specificity: underlined or boxed

Substitutions: bold

Fig. 1B



X_4 X_3 X_2 X_1 X_5 X_6

SEQ ID NO.		SEQUENCE
SEQ ID NO:22	X_1	SRFEVW
SEQ ID NO:17	X_2-X_1	WISRFEVW
SEQ ID NO:14	X_1-X_5	SRFEVWPYL
SEQ ID NO:23	$X_2-X_1-X_5-X_6$	WISRFEVWPYLKK
SEQ ID NO:12	$X_3-X_2-X_1-X_5$	GIVRKWISRFEVWPYL
SEQ ID NO:10	$X_3-X_2-X_1-X_5-X_6$	GIVRKWISRFEVWPYLKK
SEQ ID NO:24	$X_4-X_3-X_2-X_1-X_5-X_6$	ENGIVRKWISRFEVWPYLKK